WEST Search History

Hide Items | Restore | Clear | Cancel

DATE: Monday, October 16, 2006

Hide?	Set Name	Query	Hit Count
		DB=PGPB,USPT; PLUR=YES; OP=OR	
☐	L5	L4 and intron	37
☐	L4	L3 and fad2	42
☐	L3	L1 and L2	1039
☐	L2	soybean adj plant	3060
☐	L1	soybean and oleic and linoleic and linolenic	6450

END OF SEARCH HISTORY

```
RESULT 6
GMA271842
LOCUS       GMA271842                420 bp    DNA     linear   PLN 04-OCT-2000
DEFINITION  Glycine max max FAD2 gene for microsomal omego-6 desaturase, intron
            1.
ACCESSION   AJ271842
VERSION     AJ271842.1  GI:10638951
KEYWORDS    fad2 gene; microsomal omego-6 desaturase.
SOURCE      Glycine max (soybean)
  ORGANISM  Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1
  AUTHORS   Liu,Q.
  JOURNAL   Thesis (1998) University of Sydney, AUSTRALIA
REFERENCE   2  (bases 1 to 420)
  AUTHORS   Liu,Q.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-FEB-2000) Liu Q., Division of Plant Industy, CSIRO
            Australia, CSIRO Plant Industry, GPO Box 1600, Canberra, ACT 2601,
            AUSTRALIA
FEATURES             Location/Qualifiers
     source          1. .420
                     /organism="Glycine max"
                     /mol_type="genomic DNA"
                     /cultivar="Williams"
                     /db_xref="taxon:3847"
     gene            1. .420
                     /gene="FAD2"
     intron          <1. .>420
                     /gene="FAD2"
                     /number=1
ORIGIN

  Query Match             98.9%;  Score 415.2;  DB 4;  Length 420;
  Best Local Similarity   99.3%;  Pred. No. 7.5e-126;
  Matches  417;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GTAAATTAAATTGTGCCTGCACCTCGGGATATTTCATGTGGGGTTCATCATATTTGTTGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTAAATTAAATTGTGCCTGCACCTCGGGATATTTCATGTGGGGTTCATCATATTTGTTGA 60

Qy         61 GGAAAAGAAACTCCCGAAATTGAATTATGCATTTATATATCCTTTTTCATTTCTAGATTT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAAAAGAAACTCCCGAAATTGAATTATGCATTTATATATCCTTTTTCATTTCTAGATTT 120

Qy        121 CCTGAAGGCTTAGGTGTAGGCACCTAGCTAGTAGCTACAATATCAGCACTTCTCTCTATT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCTGAAGGCTTAGGTGTAGGCACCTAGCTAGTAGCTACAATATCAGCACTTCTCTCTATT 180

Qy        181 GATAAACAATTGGCTGTAATGCCGCAGTAGAGGACGATCACAACATTTCGTGCTGGTTAC 240
              ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        181 GATAAACAATTGGCTGTAATGCCGCAGTAGAAGACGATCACAACATTTCGTGCTGGTTAC 240

Qy        241 TTTTTGTTTTATGGTCATGATTTCACTCTCTCTAATCTCTCCATTCATTTTGTAGTTGTC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TTTTTGTTTTATGGTCATGATTTCACTCTCTCTAATCTCTCCATTCATTTTGTAGTTGTC 300

Qy        301 ATTATCTTTAGATTTTTCACTACCTGGTTTAAAATTGAGGGATTGTAGTTCTGTTGGTAC 360
              |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db        301 ATTATCTTTAGATTTTTCACTACCTGGTTTAAAATTGAAGGATTGTAGTTCTGTTGGTAC 360

Qy        361 ATATTACACATTCAGCAAAACAACTGAAACTCAACTGAACTTGTTTATACTTTGACACAG 420
              |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db        361 ATATTACACATTCAGCAAAACAACTGAAACTCAACTAAACTTGTTTATACTTTGACACAG 420
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OM nucleic - nucleic search, using sw model

Run on:          September 24, 2006, 12:55:25 ; Search time 3047 Seconds
                                            (without alignments)
                                            8814.544 Million cell updates/sec

Title:           US-10-606-772-2
Perfect score:   420
Sequence:        1 gtaaattaaattgtgcctgc..........ttgtttatactttgacacag 420

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters:      12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        GenEmbl:*
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                 2:  gb_pat:*
                 3:  gb_ph:*
                 4:  gb_pl:*
                 5:  gb_pr:*
                 6:  gb_ro:*
                 7:  gb_sts:*
                 8:  gb_sy:*
                 9:  gb_un:*
                 10:  gb_vi:*
                 11:  gb_ov:*
                 12:  gb_htg:*
                 13:  gb_in:*
                 14:  gb_om:*
                 15:  gb_ba:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.
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SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	420	100.0	420	2	AX088030	AX088030 Sequence
	2	420	100.0	778	2	AX088055	AX088055 Sequence
	3	420	100.0	4497	2	AX088029	AX088029 Sequence
	4	420	100.0	144984	12	AC160454	AC160454 Glycine m
	5	418.4	99.6	1852	4	AY954300	AY954300 Glycine m
	6	415.2	98.9	420	4	GMA271842	AJ271842 Glycine m
	7	211.8	50.4	2662	4	AB188251	AB188251 Glycine m
	8	199.8	47.6	405	2	AX088052	AX088052 Sequence
	9	50.2	12.0	110000	15	BX571856_26	Continuation (27 o
c	10	49.6	11.8	192929	12	AC005505	AC005505 Plasmodiu
	11	48.6	11.6	110000	15	AJ938182_24	Continuation (25 o
	12	48.6	11.6	110000	15	BA000017_25	Continuation (26 o
	13	48.6	11.6	110000	15	BA000017_26	Continuation (27 o
	14	48.6	11.6	110000	15	BA000018_25	Continuation (26 o
	15	48.6	11.6	110000	15	BA000033_25	Continuation (26 o
	16	48.6	11.6	110000	15	BX571857_25	Continuation (26 o
c	17	48	11.4	250713	13	AE014850	AE014850 Plasmodiu
c	18	47	11.2	813	2	AX620512	AX620512 Sequence
c	19	47	11.2	6435	15	AF076683	AF076683 Staphyloc
c	20	47	11.2	18355	2	AR353949	AR353949 Sequence
c	21	47	11.2	18355	2	AR535505	AR535505 Sequence
	22	47	11.2	110000	15	CP000255_25	Continuation (26 o

	23	47	11.2	110000	15	CP000046_25	Continuation (26 o
c	24	47	11.2	169794	12	AC004688	AC004688 Plasmodiu
	25	47	11.2	234081	13	PFMAL4P2	AL035475 Plasmodiu
	26	47	11.2	252650	13	AE014847	AE014847 Plasmodiu
c	27	46.4	11.0	188920	6	AL954353	AL954353 Mouse DNA
	28	44.8	10.7	168473	11	BX649544	BX649544 Zebrafish
	29	44.2	10.5	249995	13	AE014840	AE014840 Plasmodiu
c	30	44	10.5	105682	13	AC116957_3	Continuation (4 of
c	31	44	10.5	110000	12	PFMAL8P1_09	Continuation (10 o
	32	43.8	10.4	124686	12	AC087111	AC087111 Homo sapi
c	33	43.8	10.4	137502	12	AP000598	AP000598 Homo sapi
c	34	43.8	10.4	152514	12	AC021329	AC021329 Homo sapi
	35	43.8	10.4	164036	5	AP000642	AP000642 Homo sapi
c	36	43.8	10.4	167035	12	AC027116	AC027116 Homo sapi
	37	43.8	10.4	186562	12	AC011768	AC011768 Homo sapi
	38	43.6	10.4	90448	12	AC167829	AC167829 Bos tauru
	39	43.4	10.3	70373	12	AC148469	AC148469 Medicago
c	40	43.2	10.3	135090	5	HS287G14	AL033377 Human DNA
	41	43.2	10.3	135494	12	AC181945	AC181945 Strongylo
c	42	43.2	10.3	199551	12	AC006281	AC006281 Plasmodiu
	43	43.2	10.3	202803	12	AC178503	AC178503 Strongylo
c	44	43	10.2	92280	6	AL845506	AL845506 Mouse DNA
	45	43	10.2	190535	6	AC110041	AC110041 Mus muscu

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OM nucleic - nucleic search, using sw model

Run on:          September 24, 2006, 13:01:18 ; Search time 153 Seconds
                                           (without alignments)
                                         . 5136.377 Million cell updates/sec

Title:           US-10-606-772-2
Perfect score:   420
Sequence:        1 gtaaattaaattgtgcctgc..........ttgtttatactttgacacag 420

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters:      2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.
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SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	47	11.2	18355	3	US-08-956-171E-67	Sequence 67, Appl
c	2	47	11.2	18355	3	US-08-781-986A-67	Sequence 67, Appl
	3	41.8	10.0	346112	3	US-09-949-016-13165	Sequence 13165, A
	4	41.2	9.8	76269	3	US-09-949-016-14603	Sequence 14603, A
c	5	40	9.5	538	3	US-09-270-767-4382	Sequence 4382, Ap
c	6	40	9.5	538	3	US-09-270-767-19664	Sequence 19664, A
	7	40	9.5	601	3	US-09-949-016-190322	Sequence 190322,
	8	39.4	9.4	60417	3	US-09-949-016-13312	Sequence 13312, A
c	9	38.8	9.2	7963	3	US-08-956-171E-168	Sequence 168, App
c	10	38.8	9.2	7963	3	US-08-781-986A-168	Sequence 168, App
	11	38.8	9.2	255679	3	US-09-949-016-17189	Sequence 17189, A
	12	38.2	9.1	285478	3	US-09-949-016-13362	Sequence 13362, A
	13	38	9.0	48316	3	US-09-949-016-12853	Sequence 12853, A
	14	38	9.0	48316	3	US-09-949-016-13405	Sequence 13405, A
	15	37.8	9.0	7218	2	US-08-232-463-14	Sequence 14, Appl
c	16	37.8	9.0	93493	3	US-09-949-016-12063	Sequence 12063, A
c	17	37.8	9.0	95020	3	US-09-949-016-13272	Sequence 13272, A
	18	37.4	8.9	601	3	US-09-949-016-36240	Sequence 36240, A
	19	37.4	8.9	601	3	US-09-949-016-51936	Sequence 51936, A
	20	37.4	8.9	58162	3	US-09-949-016-16289	Sequence 16289, A
	21	37.4	8.9	147382	3	US-09-949-016-14624	Sequence 14624, A
	22	37.4	8.9	151256	3	US-09-949-016-12674	Sequence 12674, A
	23	37.4	8.9	151261	3	US-09-949-016-13242	Sequence 13242, A
	24	37.4	8.9	784019	3	US-09-949-016-14033	Sequence 14033, A
	25	37.4	8.9	828152	3	US-09-949-016-12777	Sequence 12777, A
c	26	37.2	8.9	832	3	US-09-621-976-2813	Sequence 2813, Ap
	27	37	8.8	1141	3	US-09-806-708B-22	Sequence 22, Appl

	28	36.8	8.8	601	3	US-09-949-016-78304	Sequence 78304, A
	29	36.8	8.8	601	3	US-09-949-016-171511	Sequence 171511,
	30	36.8	8.8	601	3	US-09-949-016-206449	Sequence 206449,
	31	36.8	8.8	6768	2	US-08-107-755A-1	Sequence 1, Appli
	32	36.8	8.8	8457	2	US-07-991-867B-1	Sequence 1, Appli
	33	36.8	8.8	8457	2	US-08-544-332-1	Sequence 1, Appli
	34	36.8	8.8	8457	3	US-09-370-861A-1	Sequence 1, Appli
	35	36.8	8.8	50000	3	US-09-662-254B-26	Sequence 26, Appl
	36	36.8	8.8	62776	3	US-09-949-016-17576	Sequence 17576, A
c	37	36.6	8.7	441	3	US-09-601-537-10	Sequence 10, Appl
c	38	36.6	8.7	1406	3	US-10-000-489-81	Sequence 81, Appl
c	39	36.6	8.7	1406	4	US-09-992-095B-81	Sequence 81, Appl
c	40	36.6	8.7	1406	5	US-10-000-986A-81	Sequence 81, Appl
c	41	36.6	8.7	4121	3	US-09-601-537-9	Sequence 9, Appli
	42	36.6	8.7	99797	3	US-09-949-016-15255	Sequence 15255, A
c	43	36.4	8.7	212139	3	US-09-949-016-16065	Sequence 16065, A
	44	36.4	8.7	260286	3	US-09-949-016-17037	Sequence 17037, A
	45	36.4	8.7	260293	3	US-09-949-016-12106	Sequence 12106, A

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OM nucleic - nucleic search, using sw model

Run on:          September 24, 2006, 13:08:22 ; Search time 1010 Seconds
                                            (without alignments)
                                            5109.710 Million cell updates/sec

Title:           US-10-606-772-2
Perfect score:   420
Sequence:        1 gtaaattaaattgtgcctgc..........ttgtttatactttgacacag 420

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters:      37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        Published_Applications_NA_Main:*
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                 2:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
                 3:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
                 4:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
                 5:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
                 6:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
                 7:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
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                 14:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
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      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	420	100.0	420	6	US-10-268-797-2	Sequence 2, Appli
2	420	100.0	420	6	US-10-268-754-2	Sequence 2, Appli
3	420	100.0	420	7	US-10-176-149-1	Sequence 1, Appli
4	420	100.0	420	8	US-10-465-800-1	Sequence 1, Appli
5	420	100.0	420	8	US-10-381-250-1	Sequence 1, Appli
6	420	100.0	420	8	US-10-606-772-2	Sequence 2, Appli
7	420	100.0	420	8	US-10-669-888A-1	Sequence 1, Appli
8	420	100.0	420	9	US-10-393-347-1	Sequence 1, Appli
9	420	100.0	420	10	US-10-518-753-1	Sequence 1, Appli
10	420	100.0	420	12	US-10-508-401A-1	Sequence 1, Appli
11	420	100.0	778	6	US-10-268-797-27	Sequence 27, Appl
12	420	100.0	778	6	US-10-268-754-27	Sequence 27, Appl
13	420	100.0	778	7	US-10-176-149-18	Sequence 18, Appl
14	420	100.0	778	8	US-10-465-800-18	Sequence 18, Appl
15	420	100.0	778	8	US-10-606-772-27	Sequence 27, Appl
16	420	100.0	778	10	US-10-518-753-18	Sequence 18, Appl
17	420	100.0	4497	6	US-10-268-797-1	Sequence 1, Appli
18	420	100.0	4497	6	US-10-268-754-1	Sequence 1, Appli
19	420	100.0	4497	7	US-10-176-149-15	Sequence 15, Appl
20	420	100.0	4497	8	US-10-465-800-15	Sequence 15, Appl
21	420	100.0	4497	8	US-10-381-250-4	Sequence 4, Appli

	22	420	100.0	4497	8	US-10-606-772-1	Sequence 1, Appli
	23	420	100.0	4497	8	US-10-669-888A-4	Sequence 4, Appli
	24	420	100.0	4497	9	US-10-393-347-4	Sequence 4, Appli
	25	420	100.0	4497	10	US-10-518-753-15	Sequence 15, Appl
	26	420	100.0	4497	12	US-10-508-401A-4	Sequence 4, Appli
	27	254	60.5	1699	8	US-10-424-599-2655	Sequence 2655, Ap
	28	199.8	47.6	405	6	US-10-268-797-24	Sequence 24, Appl
	29	199.8	47.6	405	6	US-10-268-754-24	Sequence 24, Appl
	30	199.8	47.6	405	7	US-10-176-149-2	Sequence 2, Appli
	31	199.8	47.6	405	8	US-10-465-800-2	Sequence 2, Appli
	32	199.8	47.6	405	8	US-10-381-250-2	Sequence 2, Appli
	33	199.8	47.6	405	8	US-10-606-772-24	Sequence 24, Appl
	34	199.8	47.6	405	8	US-10-669-888A-2	Sequence 2, Appli
	35	199.8	47.6	405	9	US-10-393-347-2	Sequence 2, Appli
	36	199.8	47.6	405	10	US-10-518-753-2	Sequence 2, Appli
	37	199.8	47.6	405	12	US-10-508-401A-2	Sequence 2, Appli
	38	199.8	47.6	2463	7	US-10-176-149-19	Sequence 19, Appl
	39	199.8	47.6	2463	8	US-10-465-800-19	Sequence 19, Appl
	40	199.8	47.6	2463	10	US-10-518-753-19	Sequence 19, Appl
	41	198.8	47.3	480	8	US-10-424-599-120356	Sequence 120356,
	42	56.6	13.5	1751	8	US-10-424-599-2654	Sequence 2654, Ap
c	43	48.6	11.6	816	8	US-10-282-122A-8193	Sequence 8193, Ap
c	44	47	11.2	813	3	US-09-815-242-4796	Sequence 4796, Ap
c	45	47	11.2	816	3	US-09-815-242-8829	Sequence 8829, Ap

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OM nucleic - nucleic search, using sw model

Run on:          September 24, 2006, 13:12:20 ; Search time 205 Seconds
                                             (without alignments)
                                             3621.893 Million cell updates/sec

Title:           US-10-606-772-2
Perfect score:   420
Sequence:        1 gtaaattaaattgtgcctgc..........ttgtttatactttgacacag 420

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        2335898 seqs, 883914439 residues

Total number of hits satisfying chosen parameters:      4671796

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        Published_Applications_NA_New:*
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                 2:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
                 3:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*
                 4:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*
                 5:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
                 6:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
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                 9:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
                 10:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.
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SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	420	100.0	420	7	US-11-369-993-1	Sequence 1, Appli
	2	420	100.0	420	7	US-11-376-328-1	Sequence 1, Appli
	3	420	100.0	778	7	US-11-369-993-18	Sequence 18, Appl
	4	420	100.0	4497	7	US-11-369-993-15	Sequence 15, Appl
	5	420	100.0	4497	7	US-11-376-328-4	Sequence 4, Appli
	6	199.8	47.6	405	7	US-11-369-993-2	Sequence 2, Appli
	7	199.8	47.6	405	7	US-11-376-328-2	Sequence 2, Appli
	8	199.8	47.6	2463	7	US-11-369-993-19	Sequence 19, Appl
c	9	47	11.2	813	6	US-10-471-571A-3475	Sequence 3475, Ap
c	10	43.2	10.3	135090	6	US-10-505-928-607	Sequence 607, App
	11	41.4	9.9	520	7	US-11-292-078-7699	Sequence 7699, Ap
c	12	40	9.5	1000	8	US-11-266-748A-211842	Sequence 211842,
c	13	40	9.5	1150	8	US-11-266-748A-54023	Sequence 54023, A
c	14	39.8	9.5	520	7	US-11-292-078-7699	Sequence 7699, Ap
	15	39.2	9.3	2500	6	US-10-641-321-125	Sequence 125, App
	16	39	9.3	487	7	US-11-292-078-2841	Sequence 2841, Ap
	17	39	9.3	727	8	US-11-266-748A-42816	Sequence 42816, A
c	18	39	9.3	919	6	US-10-374-780A-1356	Sequence 1356, Ap
	19	39	9.3	1000	8	US-11-266-748A-118780	Sequence 118780,
c	20	39	9.3	1000	8	US-11-266-748A-160944	Sequence 160944,
	21	39	9.3	1000	8	US-11-266-748A-293159	Sequence 293159,
c	22	39	9.3	1000	8	US-11-266-748A-344588	Sequence 344588,
	23	39	9.3	1000	8	US-11-266-748A-405069	Sequence 405069,
c	24	39	9.3	1000	8	US-11-266-748A-476115	Sequence 476115,
	25	39	9.3	1068	8	US-11-266-748A-70141	Sequence 70141, A
c	26	39	9.3	1068	8	US-11-266-748A-122952	Sequence 122952,
c	27	39	9.3	1390	8	US-11-266-748A-256869	Sequence 256869,

	28	39	9.3	1390	8	US-11-266-748A-317386	Sequence 317386,
	29	39	9.3	2026	8	US-11-266-748A-184717	Sequence 184717,
c	30	39	9.3	2321	8	US-11-266-748A-27870	Sequence 27870, A
	31	39	9.3	4098	8	US-11-266-748A-31428	Sequence 31428, A
	32	38.8	9.2	396	7	US-11-292-078-17801	Sequence 17801, A
c	33	38.8	9.2	859	8	US-11-266-748A-48163	Sequence 48163, A
	34	38.8	9.2	90537	6	US-10-669-920-1425	Sequence 1425, Ap
c	35	38.6	9.2	2434	8	US-11-266-748A-23037	Sequence 23037, A
c	36	38.4	9.1	368	7	US-11-292-078-5024	Sequence 5024, Ap
c	37	38.4	9.1	499	7	US-11-292-078-10189	Sequence 10189, A
	38	38.2	9.1	783	8	US-11-266-748A-349617	Sequence 349617,
c	39	38.2	9.1	783	8	US-11-266-748A-432996	Sequence 432996,
c	40	38.2	9.1	2578	6	US-10-700-439-70	Sequence 70, Appl
c	41	38.2	9.1	2578	8	US-11-266-748A-30590	Sequence 30590, A
	42	38.2	9.1	301477	6	US-10-539-228-456	Sequence 456, App
c	43	38	9.0	516	7	US-11-292-078-16996	Sequence 16996, A
c	44	38	9.0	537	7	US-11-292-078-8120	Sequence 8120, Ap
c	45	38	9.0	1828	8	US-11-216-545-8656	Sequence 8656, Ap

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FILE 'AGRICOLA' ENTERED AT 13:04:00 ON 16 OCT 2006

=> S INTRON AND PLANT AND REVIEW
L1            8 INTRON AND PLANT AND REVIEW

=> D L1 1-8

L1    ANSWER 1 OF 8  BIOSIS  COPYRIGHT (c) 2006 The Thomson Corporation  on STN
AN    2005:4221  BIOSIS
DN    PREV200500010147
TI    The mitochondrial DNA of land plants: peculiarities in phylogenetic
      perspective.
AU    Knoop, Volker [Reprint Author]
CS    IZMB, Univ Bonn, Kirschallee 1, D-53115, Bonn, Germany
      volker.knoop@uni-bonn.de
SO    Current Genetics, (September 2004) Vol. 46, No. 3, pp. 123-139. print.
      ISSN: 0172-8083 (ISSN print).
DT    Article
      General Review; (Literature Review)
LA    English
ED    Entered STN: 16 Dec 2004
      Last Updated on STN: 16 Dec 2004

L1    ANSWER 2 OF 8  BIOSIS  COPYRIGHT (c) 2006 The Thomson Corporation  on STN
AN    2004:272364  BIOSIS
DN    PREV200400273299
TI    Phylogenetic analysis of mealybugs (Hemiptera: Coccoidea: Pseudococcidae)
      based on DNA sequences from three nuclear genes, and a review of
      the higher classification.
AU    Downie, D. A. [Reprint Author]; Gullan, P. J.
CS    Dept Zool & Entomol, Rhodes Univ, ZA-6140, Grahamstown, South Africa
      d.downie@ru.ac.za
SO    Systematic Entomology, (April 2004) Vol. 29, No. 2, pp. 238-259. print.
      ISSN: 0307-6970 (ISSN print).
DT    Article
LA    English
ED    Entered STN: 2 Jun 2004
      Last Updated on STN: 2 Jun 2004

L1    ANSWER 3 OF 8  BIOSIS  COPYRIGHT (c) 2006 The Thomson Corporation  on STN
AN    2000:36730  BIOSIS
DN    PREV200000036730
TI    Molecular systematic studies of the Palmae.
AU    Hahn, William J. [Reprint author]
CS    CERC, Columbia University, 1200 Amsterdam Ave., 1004 Schermerhorn Ext., MC
      5557, New York, NY, 10027, USA
SO    Memoirs of the New York Botanical Garden, (1999) Vol. 83, No. 0, pp.
      47-60. print.
      CODEN: MYBGAJ. ISSN: 0077-8931.
DT    Article
      General Review; (Taxonomic Review)
LA    English
ED    Entered STN: 19 Jan 2000
      Last Updated on STN: 31 Dec 2001
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L1   ANSWER 4 OF 8 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
AN   1997:65786 BIOSIS
DN   PREV199799364989
TI   Splicing of precursors to mRNA in higher plants: Mechanism, regulation and
      sub-nuclear organisation of the spliceosomal machinery.
AU   Simpson, G. G. [Reprint author]; Filipowicz, W.
CS   John Innes Centre, Colney, Norwich NR4 7UH, UK
SO   Plant Molecular Biology, (1996) Vol. 32, No. 1-2, pp. 1-41.
      CODEN: PMBIDB. ISSN: 0167-4412.
DT   Article
      General Review; (Literature Review)
LA   English
ED   Entered STN: 11 Feb 1997
      Last Updated on STN: 11 Feb 1997

L1   ANSWER 5 OF 8 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
AN   1988:428241 BIOSIS
DN   PREV198835080371; BR35:80371
TI   VIROIDS MOLECULAR INFECTIOUS AGENTS.
AU   SMARDA J [Reprint author]
CS   DEP BIOLOGY, MED FAC, JE PURKYNE UNIV, 662 44 BRUNO CZECHOSLOVAKIA
SO   Acta Virologica, (1987) Vol. 31, No. 6, pp. 506-524.
      CODEN: AVIRA2. ISSN: 0001-723X.
DT   Article
FS   BR
LA   ENGLISH
ED   Entered STN: 24 Sep 1988
      Last Updated on STN: 24 Sep 1988

L1   ANSWER 6 OF 8 AGRICOLA Compiled and distributed by the National
      Agricultural Library of the Department of Agriculture of the United States
      of America. It contains copyrighted materials. All rights reserved.
      (2006) on STN
AN   97:33170 AGRICOLA
DN   IND20564068
TI   Splicing of precursors to mRNA in higher plants: mechanism, regulation and
      sub-nuclear organisation of the spliceosomal machinery.
AU   Simpson, G.G.; Filipowicz, W.
CS   John Innes Centre, Norwich, UK.
AV   DNAL (QK710.P62)
SO   Plant molecular biology, Oct 1996. Vol. 32, No. 1/2. p. 1-41
      Publisher: Dordrecht : Kluwer Academic Publishers.
      CODEN: PMBIDB; ISSN: 0167-4412
NTE   In the special issue: Post-transcriptional control of gene expression in
      plants/edited by W. Filipowicz and T. Hohn.
      Includes references
CY   Netherlands
DT   Article; Law
FS   Non-U.S. Imprint other than FAO
LA   English

L1   ANSWER 7 OF 8 AGRICOLA Compiled and distributed by the National
      Agricultural Library of the Department of Agriculture of the United States
      of America. It contains copyrighted materials. All rights reserved.
      (2006) on STN
AN   93:65481 AGRICOLA
DN   IND93041703
TI   RNA editing gives a new meaning to the genetic information in mitochondria
      and chloroplasts.
AU   Pring, D.; Brennicke, A.; Schuster, W.
CS   USDA, ARS, University of Florida, Gainesville, FL
AV   DNAL (QK710.P62)
SO   Plant molecular biology : an international journal on molecular biology,

biochemistry and genetic engineering, Mar 1993. Vol. 21, No. 6. p.
1163-1170
Publisher: Dordrecht : Kluwer Academic Publishers.
ISSN: 0167-4412
NTE Literature review.
Includes references.
DT Article; (SURVEY OF LITURATURE)
FS Non-U.S. Imprint other than FAO
LA English

L1 ANSWER 8 OF 8 AGRICOLA Compiled and distributed by the National
Agricultural Library of the Department of Agriculture of the United States
of America. It contains copyrighted materials. All rights reserved.
(2006) on STN
AN 92:102049 AGRICOLA
DN IND92060218
TI Regenerating good sense: RNA editing and trans splicing in plant
mitochondria.
AU Wissinger, B.; Brennicke, A.; Schuster, W.
CS Institut fur Genbiologische Forschung, Berlin, FRG
AV DNAL (QH426.T74)
SO Trends in genetics, Sept 1992. Vol. 8, No. 9. p. 322-328
Publisher: New York, N.Y. : Elsevier Science Publishers.
ISSN: 0168-9479
NTE Literature review.
Includes references.
DT Article; (SURVEY OF LITURATURE)
FS U.S. Imprints not USDA, Experiment or Extension
LA English

=> S INTRON AND PLANT
L2 1947 INTRON AND PLANT

=> S L2 AND ANTISENSE
L3 35 L2 AND ANTISENSE

=> D L3 1-35 TI

L3 ANSWER 1 OF 35 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
TI Features of Arabidopsis genes and genome discovered using full-length
cDNAs.

L3 ANSWER 2 OF 35 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
TI The Arabidopsis selenium-binding protein confers tolerance to toxic levels
of selenium.

L3 ANSWER 3 OF 35 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
TI Molecular analysis of Arabidopsis endosperm and embryo promoter trap
lines: reporter-gene expression can result from T-DNA insertions in
antisense orientation, in introns and in intergenic regions, in
addition to sense insertion at the 5 ' end of genes.

L3 ANSWER 4 OF 35 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
TI Antisense and RNAi expression for a chloroplastic superoxide
dismutase gene in transgenic plants.

L3 ANSWER 5 OF 35 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
TI Analysis of RNA-mediated gene silencing using a new vector (pKNOCKOUT) and
an in planta Agrobacterium transient expression system.

L3 ANSWER 6 OF 35 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
TI Identification of transcribed sequences in Arabidopsis thaliana by using
high-resolution genome tiling arrays.

L3 ANSWER 7 OF 35 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
TI Expression of cold-tolerant pyruvate, orthophosphate dikinase cDNA, and heterotetramer formation in transgenic maize plants.

L3 ANSWER 8 OF 35 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
TI Loss of decreased-rubisco phenotype between generations of wheat transformed with antisense and sense rbcS.

L3 ANSWER 9 OF 35 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
TI Improvement of forage quality by downregulation of maize O-methyltransferase.

L3 ANSWER 10 OF 35 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
TI Diversity of Arabidopsis genes encoding precursors for phytosulfokine, a peptide growth factor.

L3 ANSWER 11 OF 35 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
TI Mitochondrial sequence migrated downstream to a nuclear V-ATPase B gene is transcribed but non-functional.

L3 ANSWER 12 OF 35 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
TI Nodule-specific regulation of phosphatidylinositol transfer protein expression in Lotus japonicus.

L3 ANSWER 13 OF 35 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
TI Inhibition of gene expression.

L3 ANSWER 14 OF 35 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
TI Inverted-repeat DNA: A new gene-silencing tool for seed lipid modification.

L3 ANSWER 15 OF 35 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
TI Metazoan cellulase genes from termites: Intron/exon structures and sites of expression.

L3 ANSWER 16 OF 35 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
TI Seven novel methylation guide small nucleolar RNAs are processed from a common polycistronic transcript by Rat1p and RNase III in yeast.

L3 ANSWER 17 OF 35 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
TI Natural antisense transcripts of the S locus receptor kinase gene and related sequences in Brassica oleracea.

L3 ANSWER 18 OF 35 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
TI Impaired wound induction of 3-deoxy-D-arabino-heptulosonate-7-phosphate synthase and altered stem development in transgenic potato plants expressing a DAHP synthase antisense construct.

L3 ANSWER 19 OF 35 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
TI Genetic engineering of potato starch composition: Inhibition of amylose biosynthesis in tubers from transgenic potato lines by the expression of antisense sequences of the gene for granule-bound starch synthase.

L3 ANSWER 20 OF 35 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
TI Characterization of the major transcripts encoded by the regulatory MuDR transposable element of maize.

L3 ANSWER 21 OF 35 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
TI Plant pre-mRNA splicing and splicing components.

L3 ANSWER 22 OF 35 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
TI Efficient splicing of an AU-rich antisense intron sequence.

L3 ANSWER 23 OF 35 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved. (2006) on STN
TI Expression patterns of TEL genes in Poaceae suggest a conserved association with cell differentiation.

L3 ANSWER 24 OF 35 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved. (2006) on STN
TI Transgene-triggered, epigenetically regulated ectopic expression of a flower homeotic gene pMADS3 in Petunia.

L3 ANSWER 25 OF 35 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved. (2006) on STN
TI Molecular analysis of Arabidopsis endosperm and embryo promoter trap lines: reporter-gene expression can result from T-DNA insertions in antisense orientation, in introns and in intergenic regions, in addition to sense insertion at the 5' end of genes.

L3 ANSWER 26 OF 35 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved. (2006) on STN
TI Identification of transcribed sequences in Arabidopsis thaliana by using high-resolution genome tiling arrays.

L3 ANSWER 27 OF 35 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved. (2006) on STN
TI Developmental and cell-specific expression of ZWICHEL is regulated by the intron and exon sequences of its upstream protein-coding gene.

L3 ANSWER 28 OF 35 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved. (2006) on STN
TI hpRNA-mediated targeting of the Arabidopsis FAD2 gene gives highly efficient and stable silencing.

L3 ANSWER 29 OF 35 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved. (2006) on STN
TI Diversity of Arabidopsis genes encoding precursors for phytosulfokine, a peptide growth factor.

L3 ANSWER 30 OF 35 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. (2006) on STN

TI Construct design for efficient, effective and high-throughput gene silencing in plants.

L3 ANSWER 31 OF 35 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. (2006) on STN

TI Nodule-specific regulation of phosphatidylinositol transfer protein expression in Lotus japonicus.

L3 ANSWER 32 OF 35 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. (2006) on STN

TI A prolonged cold treatment-induced cytochrome P450 gene from Arabidopsis thaliana.

L3 ANSWER 33 OF 35 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. (2006) on STN

TI De novo purine synthesis in Arabidopsis thaliana. II. The PUR7 gene encoding 5'-phosphoribosyl-4-(N-succinocarboxamide)-5-aminoimidazole synthetase is expressed in rapidly dividing tissues.

L3 ANSWER 34 OF 35 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. (2006) on STN

TI Impaired wound induction of 3-deoxy-D-arabino-heptulosonate-7-phosphate (DAHP) synthase and altered stem development in transgenic potato plants expressing a DAHP synthase antisense construct.

L3 ANSWER 35 OF 35 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. (2006) on STN

TI Characterization of the major transcripts encoded by the regulatory MuDR transposable element of maize.

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L3 ANSWER 28 OF 35 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. (2006) on STN

AN 2003:34634 AGRICOLA

DN IND23324111

TI hpRNA-mediated targeting of the Arabidopsis FAD2 gene gives highly efficient and stable silencing.

AU Stoutjesdijk, P.A.; Singh, S.P.; Liu, Q.; Hurlstone, C.J.; Waterhouse, P.A.; Green, A.G.

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AV    DNAL (450 P692)
SO    Plant physiology, Aug 2002. Vol. 129, No. 4. p. 1723-1731
      CODEN: PLPHAY; ISSN: 0032-0889
NTE   Includes references
CY    Maryland; United States
DT    Article; Conference
FS    Other US
LA    English

L3    ANSWER 30 OF 35  AGRICOLA  Compiled and distributed by the National
      Agricultural Library of the Department of Agriculture of the United States
      of America.  It contains copyrighted materials.  All rights reserved.
      (2006) on STN
AN    2002:26817  AGRICOLA
DN    IND23262705
TI    Construct design for efficient, effective and high-throughput gene
      silencing in plants.
AU    Wesley, S.V.; Helliwell, C.A.; Smith, N.A.; Wang, M.; Rouse, D.T.; Liu,
      Q.; Gooding, P.S.; Singh, S.P.; Abbott, D.; Stoutjesdijk, P.A.; Robinson,
      S.P.; Gleave, A.P.; Green, A.G.; Waterhouse, P.M.
AV    DNAL (QK710.P68)
SO    The Plant journal : for cell and molecular biology, Sept 2001. Vol. 27,
      No. 6. p. 581-590
      Publisher: Oxford : Blackwell Sciences Ltd.
      ISSN: 0960-7412
NTE   Includes references
CY    England; United Kingdom
DT    Article
FS    Non-U.S. Imprint other than FAO
LA    English


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